

AMENDMENTS TO THE CLAIMS

1. (Original) A method of quantifying the absolute or relative number of molecules present in a sample after carrying out an analysis procedure on the sample, comprising the steps of:

(i) attaching a unique molecular tag to substantially all of the molecules in the sample;

(ii) carrying out the analysis procedure using the molecules of the sample; and

(iii) on the basis of the molecular tags determining the absolute or relative number of molecules present in the original sample which underwent the analysis procedure.

2. (Original) A method according to claim 1, further comprising, either before or after analysis, the step of incorporating into the molecular tag a sample identification portion.

3. (Currently amended) A method according to claim 1 ~~or claim 2~~, wherein step (iii) is carried out by identifying the tag in a read-out step.

4. (Original) A method according to claim 3, wherein the read-out step is carried out in a manner that ensures that each tag in the original sample is read at least once.

5. (Currently amended) A method according to ~~any preceding~~ claim 1, wherein the molecules are polymer molecules.

6. (Currently amended) A method according to ~~any preceding~~ claim 1, wherein the sample comprises different molecules.

7. (Currently amended) A method according to ~~any preceding~~ claim 1, wherein the sample comprises multiple molecules of the same type.

8. (Currently amended) A method according to ~~any preceding claim 1~~, wherein the molecular tag is or comprises a polynucleotide molecule of defined sequence.

9. (Original) A method according to claim 8, wherein the polynucleotide is a DNA molecule of defined sequence.

10. (Currently amended) A method according to ~~any of claims 1 to 7~~ claim 1, wherein the molecular tag is or comprises an antibody.

11. (Currently amended) A method according to ~~any of claims 1 to 7 or claim 10~~ claim 1, wherein the molecular tag is or comprises an aptamer.

12. (Currently amended) A method according to ~~any of claims 1 to 7~~ claim 1, wherein the molecular tags are polynucleotides and the analysis procedure involves an amplification reaction.

13. (Currently amended) A method according to ~~any of claims 1 to 8~~ claim 1, wherein the polynucleotide tags are amplified in a polymerase reaction.

14. (Original) A method according to claim 13, wherein the molecules are polynucleotides and the analysis procedure involves an amplification of the polynucleotide molecules.

15. (Original) A method according to claim 14, wherein two or more polynucleotide molecular tags are bound to each target polynucleotide, and said tags subsequently ligated together and the resulting ligated polynucleotide amplified in a polynucleotide amplification reaction.

16. (Currently amended) A method according to ~~any preceding claim 1~~, wherein the analysis procedure involves nano-pore detection.

17. (Currently amended) A method according to ~~any preceding claim~~, claim 1, wherein the molecular tag, or a part of the molecular tag, indicates the sample-origin of the tagged molecule.

18. (Currently amended) A method according to ~~any preceding claim~~ claim 1, wherein the results of step (iii) are collated in a computer programme.

19. (Currently amended) A method according to ~~any preceding claim~~ claim 1, wherein the molecules are proteins.

20. (Original) A method according to claim 18, wherein the molecules are antibodies.

21. (Original) A method for detecting the presence of a molecule in a sample, comprising contacting the sample with two or more molecule-binding moieties each having affinity for different parts of the target molecule, wherein the moieties comprise a polynucleotide molecular tag and wherein, on binding of at least two moieties to the target molecule, two or more molecular tags are ligated in a subsequent ligation step, and the ligated polynucleotide detected, characterised in that the ligated polynucleotide comprises a sequence that identifies the class of target molecule and the individual molecule.

22. (Currently amended) A method according to claim 21, wherein the ligated polynucleotide further comprises a sample identification portion.

23. (Original) A method for detecting the presence of specific molecules present on the outer-surface of a cell or membrane, comprising:

(i) contacting the cell or membrane with a sample comprising different molecule-targeting moieties, each moiety comprising a polynucleotide molecular tag of defined sequence;

(ii) carrying out a ligation reaction to ligate adjacent polynucleotides; and

(iii) detecting the ligated polynucleotide(s) and determining the presence of the outer-surface or membrane molecules;

wherein the polynucleotide molecular tags comprise a nucleotide sequence that identifies the class of outer-surface molecule and optionally the individual molecule.

24. (Original) A method according to claim 23, wherein the polynucleotide molecular tag further comprises a sample identification portion.

25. (Original) A method according to claim 19 or claim 20, wherein the outer surface molecule is a protein, and the moiety is a protein-binding molecule.

26. (Currently amended) A method according to any one of claims 8, 9 or 21 to ~~25~~ 23, wherein the polynucleotide molecular tag comprises a sequence of nucleotides representing distinct units of binary code.

27. (Original) A method for determining the sequence of a polynucleotide in a sample, comprising the steps of:

- i) attaching a unique molecular tag to polynucleotides in the sample;
- ii) amplifying the polynucleotides;
- iii) fragmenting the amplified polynucleotides; and
- iv) sequencing at least those fragmented polynucleotides that comprise a molecular tag and identifying the molecular tag wherein, on the basis of the molecular tags, the sequence information for each individual polynucleotide is collated.

28. (Currently amended) A method according to claim 27, wherein the molecular tag is as defined in any one of claims 9 to 12 ~~and~~ or claim 17.

29. (Original) A method according to claim 22 or claim 23, wherein the sequencing step comprises converting the sequence information into magnifying tags, each tag representing one base in the polynucleotide.

30. (Currently amended) A method according to any one of claims 22 to 24, wherein the results of step (iv) are collated in a computer programme.

31. (Original) A method for determining the sample origin of a biological molecule, comprising labelling the biological molecule with a molecular tag that is specific for the sample from which the molecule was taken or placed into, wherein, the sample origin is determined by identifying the molecular tag.

32. (Currently amended) A method according to claim 31, wherein the molecular tag is as defined in any one of claims 9 to 12 ~~and~~ or claim 17.

33. (Currently amended) A kit comprising a discrete compartment comprising one or more molecular tags as defined in any one of claims 9 to 12 ~~and~~ or claim 17.